

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2003, 16:38:32 ; Search time 19 seconds
(without alignments)
1315.524 Million cell updates/sec

Title: US-09-840-243B-11

Perfect score: 1341
Sequence: 1 MULTIPARADILQTCRPPASE.....VIENHILKLFQSNLVPADPE 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 73:*

1: piri:***
2: piri2:***
3: piri3:***
4: piri4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219.5	16.4	426	2 AE2149	hypothetical prote
2	214	16.0	2039	2 T15347	ankyrin-related un
3	207.5	15.5	1031	2 T43458	hypothetical prote
4	202.5	15.1	3924	2 G37431	ankyrin 2, neuroma
5	193	14.4	4377	2 A55575	ankyrin 3, long sp
6	189	14.1	1001	2 G30385	G9a protein - huma
7	188.5	14.1	1765	2 T42714	ankyrin 3, splice
8	188.5	14.1	1940	2 T42715	ankyrin 3, splice
9	188.5	14.1	1943	2 T42716	ankyrin 3, splice
10	188.5	14.1	1961	2 T42716	ankyrin 3, splice
11	184	13.7	1881	1 G37771	ankyrin 1, erythro
12	183	13.6	1848	2 S37771	ankyrin 1, erythro
13	183	13.6	1862	2 T49502	ankyrin 1, mouse
14	182	13.6	1856	2 B35049	ankyrin 1, erythro
15	182	13.6	1880	2 A35049	ankyrin 1, erythro
16	181.5	13.5	1549	2 T13940	ankyrin 1, fruit fl
17	176.5	13.2	2584	2 T21558	hypothetical prote
18	176.5	13.2	2606	2 T21557	hypothetical prote
19	175	13.0	495	2 T27995	hypothetical prote
20	173.5	12.9	888	2 D84650	probable potassium
21	173	12.9	333	2 UC7713	ankyrin-repeat pro
22	172.5	12.9	1188	2 T15552	hypothetical prote
23	171.5	12.8	741	2 A45771	2-5a-dependent RNA
24	171	12.8	1398	2 T21884	hypothetical prote
25	169.5	12.6	1062	2 T14151	inv protein - mous
26	167	12.5	211	2 T18174	ankyrin repeat pro
27	166.5	12.4	1062	2 T10255	inversin - mouse
28	166	12.4	658	2 S68418	protein phosphatas
29	165.5	12.3	451	1 S68418	serine/threonine-s

ALIGNMENTS

30	164	12.2	642	2 S68154	hypothetical prote
31	163	12.2	118	2 A54412	V-1 protein - rat
32	163	12.2	319	2 A54291	cytokine inducible
33	163	12.2	439	2 J01729	ankyrin-repeat pro
34	163	12.2	1401	2 S11527	alpha-latrotoxin p
35	162	12.1	656	2 A34793	sex-determining pr
36	162	12.1	1004	2 A51442	myosin-light-chain
37	160	11.9	815	2 JG0197	myosin-light-chain
38	159.5	11.9	1023	2 T26261	hypothetical prote
39	158.5	11.8	347	2 C40858	GA-binding protein
40	158.5	11.8	382	2 B40858	GA-binding protein
41	157.5	11.7	662	2 E94725	ankyrin-like prote
42	157.5	11.7	347	2 C46146	nuclear respirator
43	156.5	11.7	348	2 I38744	nuclear respirator
44	156.5	11.7	360	2 I38743	nuclear respirator
45	156.5	11.7	395	2 I38741	nuclear respirator

RESULT 1

AE2149
hypothetical protein all12748 [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C/Accession: AE2149

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriuch

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8: 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A/Reference number: AB1807; MUID:21595285; PMID:11759640

A/Accession: AE2149

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1426 <KIR>

A/Cross-references: GB:BA000019; PIDN:BA074447.1; PID:G17131841; GSPDB:GN00179

A/Experimental source: strain PCC 7120

C/Genetics:

A/Gene: all12748

Query Match 16.4% Score 219.5; DB 2; Length 426;
Best Local Similarity 30.7%; Pred. No. 4.6e-10;
Matches 62; Conservative 34; Mismatches 71; Indels 35; Gaps 4;

QY	62	QAGSLKHSSTL-----	-----TNRQGNVSAIPATLDSUSTHQLAAGSLDQK 107
DB	234	QDGEALHLATVEGVVDVVLNGANTQIKRLGDPPLVAALQGH-----	-----DQIV 285
QY	108	EHRR-----	-----GDNLVNKPDERGFPLIWAASAFGEIETVRFPLEWGADPHILAKRESAL 161
DB	286	ETLLRYGANVHGDNL-----	-----GEPPLTLAASQGTATVRIILDGAGANNIPASGKTL 338
QY	162	SIASGVTIDIVGLLENDVDINIDVWNGGTPPLVAAGNHVCVEALARGADLTTEAD 221	
DB	339	IKATRNHEGVQLLLAKGANVYDSGATLIMAAAGNVKVVQILLEGADNLKNR 398	
QY	222	SGYTPMDLVAALGVRRVOQVIE 243	
DB	399	GGYTLMLIAEFNGFRSIVQILK 420	

RESULT 2

T15347
ankyrin-related unc-44 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Aug-2002

C/Accession: T15347; T15346; T15345; A57282; B57282; C57282

R/Gatung, S.

submitted to the EMBL Data Library, February 1996

A/Description: The sequence of C. elegans cosmid B0350.

A/Reference number: Z18332

A:Accession: T15347
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2039 <GAT>
 A:Cross-references: EMBL:US0071; NID:g1208871; PID:g1208873; PIDN:AAA93443.1
 A:Accession: T15346
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1000, 'SKLQHT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQR', 1950, 'IVA
 32, 'S', 2034-2035, 'GPTRRSVPEEHRHSHEDHSGT' <GA2>
 A:Cross-references: EMBL:US0071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1
 A:Accession: T15344
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'QRSTIVAESESTSEQVE', 1934-1935, 'E
 <GA3>
 A:Cross-references: EMBL:US0071; NID:g1208871; PID:g1208874; PIDN:AAA93444.1
 A:Accession: T15345
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQR', 1950, 'IVAES', 1956-1957, 'EQVE
 PTRRSVEPEHRHSHEDHSGT' <GA4>
 A:Cross-references: EMBL:US0071; NID:g1208871; PID:g1208876; PIDN:AAA93446.1
 R:Otsuka, A.J.; Franco, R.; Yang, B.; Shim, K.H.; Tang, U.Z.; Zhang, Y.Y.; Boontrakulpo
 J. Cell Biol. 129, 1081-1092, 1995
 A:Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in *Cae*
 A:Reference number: A57282; MUID:95263663; PMID:7744957
 A:Accession: A57282
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-852, 'GGG', 856-1000, 'SKLQHT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWE
 'SHRED', 2007-2008, 'TY', 2011, 2017, 'TT', 2020-2022, 'SHIS' <OTS>
 A:Cross-references: GB:U01734; NID:9790607; PIDN:AAA85854.1; PID:9790608
 A:Accession: B57282
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E
 V', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPTRRSVEPEHRHS', 1984-1985, 'EDHSGS', 1
 A:Cross-references: GB:U01731
 A:Accession: C57282
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 194, 'F', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'O', 414, 824, 'S', 826, 'ER', 829, '4
 4, 'TIV', 1828, 'ESTS', 1833, 'OV', 1836, 'E', 1934-1935, 'EES', 1939, 'REDDGTTVT', 194
 C:Genetics: GB:U01732; NID:9790603; PIDN:AAA85853.1; PID:9790604
 A:Gene: C57P:unc-44
 A:Intons: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979
 C:Superfamily: ankyrin; ankyrin repeat homology
 F:164-192/Domain: ankyrin repeat homology <AND>
 F:358-390/Domain: ankyrin repeat homology <ANI>
 F:391-423/Domain: ankyrin repeat homology <ANI1>
 Query Match 16.8%; Score 214; DB 2; Length 2039;
 Best Local Similarity 27.3%; Pred. No. 1.2e-08;
 Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;
 19 SELGDDPEPGEADGDTVLSFPCPEPVPNPDPDASVSSPQAGSSLKHSSTLTNROR 78
 2 SNEGDPPPOQOQPSQVQA---PAAPPEPGRAE----- 32
 79 GNEVSALPATLDSLSIHLAAGELDOKEHRLKGDNLVNRKPDDEGFTPLIWASAFGEIE 138
 33 -----GSASFPLRAAAGDLEKVLRLAAGTD-INTSNANGLSLHLASKEGHS 80
 139 TVRPLEMGADPHILAKERESALSTAGGYTDIVGLLERPVDINITYDMNGTPLLAV 198
 81 VRELIRKQAVDADRKTGNTALHSLASGSLITVILVENGANVNVOSVNGFTPLVMA 140
 199 RGNHVKCEBALIARGADLTTEADSGYTMDLAVNLGY-RKYQOVLEN 244
 141 QENHEEVYKILKGAQNALSTEDGFTPLVALAQQGHDRVAVVLEN 187

RESULT 3
 T43458
 hypothetical protein DKFZp434F0621.1 - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
 C:Accession: T43458
 R:Blum, H.; Baurerachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: 222517
 A:Accession: T43458
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1031 <AAA>
 A:Cross-references: EMBL:AL133620
 A:Experimental source: adult testis; clone DKFZp434F0621
 C:Genetics:
 A:Note: DKFZp434F0621.1

Query Match 15.5%; Score 207.5; DB 2; Length 1031;
 Best Local Similarity 34.5%; Pred. No. 1.5e-08;
 Matches 51; Conservative 34; Mismatches 60; Indels 3; Gaps 3;
 100 QGELDQLEKHLRKGDNLVNRKPDDEGFTPLIWASAFGEIEVFLFEMGADPHILAKERES 159
 81 EGHVHIVEILKCGVNLHR-DMGWTALMMAACYGRDVLVHLSHGANSVTLQSV 139
 160 ALSIASFG-GYTDIVGLLERPVDINITYDMNGTPLLAVRGNHVKCEBALIARGADLT 218
 140 YPIIWAARGHADIVHLLQNGAKVNCSDKYGTTPLVWAARKGHLECVHLLAMGADV 199
 219 EADSGYTPMDLAVNLGY-RKYQOVLEN 245
 200 EGANSMTALIVAVGSGTQSVKEILKRN 227

RESULT 4
 S37431
 ankyrin 2, neuronal long splice form - human
 N:Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
 R:Chan, W.
 submitted to the EMBL Data Library, September 1993
 A:Reference number: S37431
 A:Accession: S37431
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-3924 <CHA>
 A:Cross-references: EMBL:Z26634; NID:9406287; PIDN:CA81387.1; PID:9406288
 R:Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
 J. Cell Biol. 114, 241-253, 1991
 A:Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
 A:Reference number: A39643; MUID:91302466; PMID:1830053
 A:Accession: A39643
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2077 <ORT>
 A:Cross-references: GB:X56957
 A:Accession: B39643
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1443, 3585-3924 <OTT>
 A:Cross-references: EMBL:X56958
 R:Use, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,
 Genomics 10, 858-866, 1991
 A:Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
 A:Reference number: A40334; MUID:92009921; PMID:1833308
 A:Accession: A40334
 A:Molecule type: DNA
 A:Residues: 463-474, 'EE', 477-495 <TSE>

A:Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
 R:Chan, W.; Kordeli, E.; Bennett, V.
 J. Cell Biol. 123, 1463-1473, 1993
 A:Title: 440-kD ankyrinb: structure of the major developmentally regulated domain and se
 A:Reference number: A49462; MUID:94075409; PMID:8253844
 A:Accession: A49462
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 13924 <RES>
 A:Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
 C:Genetics:
 A:Gene: GDB:ANK2
 A:Cross-references: GDB:127607; OMIM:106410
 A:Map position: 4q25-4q27
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 F:2-3924/Product: ankyrin 2, long form #status predicted <MA1>
 F:2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
 F:63-95/Domain: ankyrin repeat homology <AN01>
 F:66-128/Domain: ankyrin repeat homology <AN02>
 F:129-161/Domain: ankyrin repeat homology <AN03>
 F:162-190/Domain: ankyrin repeat homology <AN04>
 F:191-223/Domain: ankyrin repeat homology <AN05>
 F:232-264/Domain: ankyrin repeat homology <AN06>
 F:265-297/Domain: ankyrin repeat homology <AN07>
 F:298-330/Domain: ankyrin repeat homology <AN08>
 F:331-363/Domain: ankyrin repeat homology <AN09>
 F:364-396/Domain: ankyrin repeat homology <AN10>
 F:397-429/Domain: ankyrin repeat homology <AN11>
 F:430-462/Domain: ankyrin repeat homology <AN12>
 F:463-495/Domain: ankyrin repeat homology <AN13>
 F:496-528/Domain: ankyrin repeat homology <AN14>
 F:529-561/Domain: ankyrin repeat homology <AN15>
 F:562-594/Domain: ankyrin repeat homology <AN16>
 F:595-627/Domain: ankyrin repeat homology <AN17>
 F:628-660/Domain: ankyrin repeat homology <AN18>
 F:661-693/Domain: ankyrin repeat homology <AN19>
 F:694-726/Domain: ankyrin repeat homology <AN20>
 F:727-759/Domain: ankyrin repeat homology <AN21>
 F:760-792/Domain: ankyrin repeat homology <AN22>
 F:793-825/Domain: ankyrin repeat homology <AN23>
 Query Match 15.1%; Score 202.5; DB 2; Length 3924;
 Best Local Similarity 29.3%; Pred. No. 2,6e-07;
 Matches 56; Conservative 43; Mismatches 81; Indels 11; Gaps 4;

QY 55 DASVSPQAGSLKSTTTNRQNGEVSAIPATLDSIHQLAAGELDQKEHRLKXD 114
 DB 5 DAAOKS-DSGEKFNSSQRRKPKKSDSNA-----SFLRAARAGNDKVEYELKGI 55
 QY 115 NLVNRDEGFPLIWAFAFGEIETVRFLLEWQADPHILAKERESALSLASTGTYDI 174
 DB 56 D-INTCQNGLNALHLAAKEGHVGLVQELLGRSSVDSATKKNLTALHIALAGQAEVVK 114
 QY 175 LLLEKDVNINIDMNGTPLLVAVRGNHVKCYEALLARGADLTTEADSGYTPMDLAVALG 234
 DB 115 VLVEKGANINAGQNGFTPLVMAAGENHIDVVKYLLLENGANOSTATEDGFTPLAVALQ 174
 QY 235 YRK-VQGVLEN 244
 DB 175 HNOAVAILLEN 185

RESULT 5
 ASS575
 ankyrin 3, long splice form - human
 N:Alternate names: ankyrin G
 C:Species: Homo sapiens (man)
 C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 20-Sep-1999
 C:Accession: A55575
 R:Kordeli, E.; Lambert, S.; Bennett, V.
 U. Biol. Chem. 270, 2352-2359, 1995
 A:Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the ax

A:Reference number: A55575; MUID:95138209; PMID:7836469
 A:Accession: A55575
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-4377 <KOR>
 A:Cross-references: GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025
 C:Genetics:
 A:Gene: GDB:ANK3
 A:Cross-references: GDB:424503; OMIM:600465
 A:Map position: 10q21-10q21
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
 C:Keywords: alternative splicing; peripheral membrane protein
 F:73-105/Domain: ankyrin repeat homology <AN01>
 F:106-138/Domain: ankyrin repeat homology <AN02>
 F:139-171/Domain: ankyrin repeat homology <AN03>
 F:172-200/Domain: ankyrin repeat homology <AN04>
 F:201-233/Domain: ankyrin repeat homology <AN05>
 F:234-266/Domain: ankyrin repeat homology <AN06>
 F:267-299/Domain: ankyrin repeat homology <AN07>
 F:300-332/Domain: ankyrin repeat homology <AN08>
 F:333-365/Domain: ankyrin repeat homology <AN09>
 F:366-398/Domain: ankyrin repeat homology <AN10>
 F:399-431/Domain: ankyrin repeat homology <AN11>
 F:432-464/Domain: ankyrin repeat homology <AN12>
 F:465-497/Domain: ankyrin repeat homology <AN13>
 F:498-530/Domain: ankyrin repeat homology <AN14>
 F:531-563/Domain: ankyrin repeat homology <AN15>
 F:564-596/Domain: ankyrin repeat homology <AN16>
 F:597-629/Domain: ankyrin repeat homology <AN17>
 F:630-662/Domain: ankyrin repeat homology <AN18>
 F:663-695/Domain: ankyrin repeat homology <AN19>
 F:696-728/Domain: ankyrin repeat homology <AN20>
 F:729-761/Domain: ankyrin repeat homology <AN21>
 F:762-794/Domain: ankyrin repeat homology <AN22>
 F:795-827/Domain: ankyrin repeat homology <AN23>
 Query Match 14.4%; Score 193; DB 2; Length 4377;
 Best Local Similarity 28.1%; Pred. No. 1.8e-06;
 Matches 50; Conservative 43; Mismatches 75; Indels 10; Gaps 3;

QY 68 KHSITLTNRQNGEVSAIPATLDSIHQLAAGELDQKEHRLKXDNLVNRPDEGF 127
 DB 27 KHRKRSRDKKSDSNA-----SYLPAARAGHLEKALDYIKNGVD-INTCQNGLNA 77
 QY 128 LIIWASAFGEIETVRFLLEWQADPHILAKERESALSLASTGTYDIYGLLEKDVNINID 187
 DB 78 LHLASKEGHVEVSEILQREANVDAATKKNTALHIALAGAEVVKVLTNGCANAGS 137
 QY 188 YNGGTPPLVAVRGNHVKCYEALLARGADLTTEADSGYTPMDLAVALGY-RKYQGVLEN 244
 DB 138 QNGFTPLVMAAGENHIDVVKYLLLENGASOSLATEDGFTPLAVALQGHQVSLLEN 195

RESULT 6
 S30385
 G9a protein - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S30385
 R:Milner, C.M.; Campbell, R.D.
 Biochem. J. 290, 811-818, 1993
 A:Title: The G9a gene in the human major histocompatibility complex encodes a novel prot
 A:Reference number: S30385; MUID:93207535; PMID:8457211
 A:Accession: S30385
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1001 <ML>
 A:Cross-references: EMBL:X69838; NID:g287864; PIDN:CAA49491.1; PID:g287865
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
 F:441-673/Domain: ankyrin repeat homology <ANR>
 Query Match 14.1%; Score 189; DB 2; Length 1001;
 Best Local Similarity 35.3%; Pred. No. 4.6e-07;

Matches 49; Conservative 18; Mismatches 72; Indels 0; Gaps 0;

QY 91 SLSTHOLAQGEIDQLKEHRLKGNLVNKKPBERGFTPLIMASAFGEITVFLWEGADP 150
 Db 543 STCLHHAQKIGNLEWVLLSTGVVDVAQSGWTPITMAEHKHEIVIRMLTRGADV 602
 QY 151 HILAKERESALSLASTGYTDIVGLLERVDVINIYDWNNGSTPLLYAVRGNNKVCVEALL 210
 Db 603 TLTNDNEENICLHMASFPGSAIAIEVLLNARCDELHVAHVHGTPLHIAARESHYDVCVLLFL 662
 QY 211 ARGADLTTEADSGVTTPMDL 229
 Db 663 SRGANPELKNKEGDTAWDL 681

RESULT 7

T42714
 ankyrin 3, splice form 2 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C/Accession: T42714
 R/Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, J.
 J. Cell Biol. 130, 313-330, 1995
 A/Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.
 A/Reference number: Z22237; MUID:95340633; PMID:7615634
 A/Accession: T42714
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1765 <PEP>
 A/Cross-references: EMBL:L40632; NID:g710548; PID:g710551; PIDN:AA801605.1
 A/Experimental source: strain C57BL/6J; kidney
 C/Genetics:
 A/Gene: Ank3
 A/Map position: 10
 A/Intons: 1587/1
 C/Superfamily: ankyrin; ankyrin repeat homology
 C/Keywords: alternative splicing

Query Match 14.1%; Score 188.5; DB 2; Length 1765;
 Best Local Similarity 25.5%; Pred. No. 1.1e-06;
 Matches 62; Conservative 43; Mismatches 77; Indels 61; Gaps 6;

QY 62 QAGSLKSTT-----LTNRQGNVSALEPATLD---SLST-----HQLAAGE 102
 Db 503 QQGASPNATTSCTGYTPHLAAREGHEVDAAFLDHDGASISITTKGFTPLHVAAYGK 560
 QY 103 LDQKEHLRKGDNLVKNRPD-----PDAAGKSGITPLHVAHYDNOKVALLLDQASPHAAKNGYT 126
 Db 561 LEVASLLQKAS----PDAAGKSGITPLHVAHYDNOKVALLLDQASPHAAKNGYT 616
 QY 127 PLIVASAFGEITVFLWEGADPHILAKERESALSLASTGYTDIVGLLERVDVINIY 186
 Db 617 PLHTAAKNQMDIATSLLEYGADANAATRGIAVHLAOGSHVDMVSLLSRNANVNIS 676
 QY 187 DMNGTPLLYAVRGNNKVCVEALLARGADLTTEADSGTTPMDLAVALGRKQVQVIEHHI 246
 Db 677 NKSGITPLHLLAAGEBRVAVAEVLVNOGAHVDAQTNGYTPHVGCHYGNIKIVNFIQHS 736
 QY 247 LKT 249
 Db 737 AKV 739

RESULT 8

T42715
 ankyrin 3, splice form 3 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C/Accession: T42715
 R/Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, J.
 J. Cell Biol. 130, 313-330, 1995
 A/Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene

the repeat domain.
 A/Reference number: Z22237; MUID:95340633; PMID:7615634
 A/Accession: T42715
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1940 <PEP>
 A/Cross-references: EMBL:L40632; NID:g710548; PID:g710549; PIDN:AA801604.1
 A/Experimental source: strain C57BL/6J; kidney
 C/Genetics:
 A/Gene: Ank3
 A/Map position: 10
 A/Intons: 834/1
 C/Superfamily: ankyrin; ankyrin repeat homology
 C/Keywords: alternative splicing

Query Match 14.1%; Score 188.5; DB 2; Length 1940;
 Best Local Similarity 25.5%; Pred. No. 1.3e-06;
 Matches 62; Conservative 43; Mismatches 77; Indels 61; Gaps 6;

QY 62 QAGSLKSTT-----LTNRQGNVSALEPATLD---SLST-----HQLAAGE 102
 Db 503 QQGASPNATTSCTGYTPHLAAREGHEVDAAFLDHDGASISITTKGFTPLHVAAYGK 560
 QY 103 LDQKEHLRKGDNLVKNRPD-----PDAAGKSGITPLHVAHYDNOKVALLLDQASPHAAKNGYT 126
 Db 561 LEVASLLQKAS----PDAAGKSGITPLHVAHYDNOKVALLLDQASPHAAKNGYT 616
 QY 127 PLIVASAFGEITVFLWEGADPHILAKERESALSLASTGYTDIVGLLERVDVINIY 186
 Db 617 PLHTAAKNQMDIATSLLEYGADANAATRGIAVHLAOGSHVDMVSLLSRNANVNIS 676
 QY 187 DMNGTPLLYAVRGNNKVCVEALLARGADLTTEADSGTTPMDLAVALGRKQVQVIEHHI 246
 Db 677 NKSGITPLHLLAAGEBRVAVAEVLVNOGAHVDAQTNGYTPHVGCHYGNIKIVNFIQHS 736
 QY 247 LKT 249
 Db 737 AKV 739

RESULT 9

T42713
 ankyrin 3, splice form 1 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C/Accession: T42713
 R/Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, J.
 J. Cell Biol. 130, 313-330, 1995
 A/Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.
 A/Reference number: Z22237; MUID:95340633; PMID:7615634
 A/Accession: T42713
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1943 <PEP>
 A/Cross-references: EMBL:L40632; NID:g710548; PID:g710550; PIDN:AA801606.1
 A/Experimental source: strain C57BL/6J; kidney
 C/Genetics:
 A/Gene: Ank3
 A/Map position: 10
 A/Intons: 855/1
 C/Function:
 A/Description: supposed to play an important role in the polarized distribution of many
 A/Note: major kidney ankyrin
 C/Superfamily: ankyrin; ankyrin repeat homology
 C/Keywords: alternative splicing

Query Match 14.1%; Score 188.5; DB 2; Length 1943;
 Best Local Similarity 25.5%; Pred. No. 1.3e-06;
 Matches 62; Conservative 43; Mismatches 77; Indels 61; Gaps 6;

QY 62 QAGSLKSTT-----LTNRQGNVSALEPATLD---SLST-----HQLAAGE 102
 Db 503 QQGASPNATTSCTGYTPHLAAREGHEVDAAFLDHDGASISITTKGFTPLHVAAYGK 560

Db 503 QOQASPNAAATTSYGTPLHLAAREGHEVAAAF--LLDHGASLSITTKGFTPLHVAARYK 560
OY 103 LDQKEHLRKGDNLVVKPD-----ERGFT 126
Db 561 LEVASLLLOKAS----PDAACKSGTLPLHVAHYNDQKVALLLDQASPHAAANGYT 616
OY 127 PLIWAASAGEIETVRFLEWGDPHILAKERESALSLASTGYTDIVGLLEBRVDINITY 186
Db 617 PLHIAAKKQMDIATSLLEYGADANAATROGIAVHLAAQEGHVDWVSLLSRNANVLS 676
OY 187 DMNGSTPLIYAVRGHNVKCEVALLARGADLTTEADSGTTPMOLAVAGYRKQOVENHI 246
Db 677 NKSGTLPLHIAAQEDRVNAEVLVNOGAHVDAQTCKGYTPLHVCHYGNIKIVNLLQHS 736
OY 247 LKL 249
Db 737 AKV 739

RESULT 10
T42716
ankyrin 3, splice form 4 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C/Accession: T42716
J. Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
R. Cell Biol. 130, 313-330, 1995
A>Title: Anky (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A/Reference number: Z22237, MUID:95340633, PMID:7615634
A/Accession: T42716
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1961 <PRT>
A/Cross-references: EMBL:LA0632, NID:G710548, PID:G710552, PIDN:AB01607.1
A/Experimental source: Strain C57BL/6J; Kidney
A/Genetics:
A/Map position: 10
C/Superfamily: ankyrin; ankyrin repeat homology
C/Keywords: alternative splicing

Query Match 14.1%; Score 188.5; DB 2; Length 1961;
Best Local Similarity 25.5%; Pred. No. 1.3e-06;
Matches 62; Conservative 43; Mismatches 77; Indels 61; Gaps 6;
OY 62 QAGSLKXSTT-----LTNRQGNVEGALPATLD---SLST-----HQLAAGE 102
Db 503 QOQASPNAAATTSYGTPLHLAAREGHEVAAAF--LLDHGASLSITTKGFTPLHVAARYK 560
OY 103 LDQKEHLRKGDNLVVKPD-----ERGFT 126
Db 561 LEVASLLLOKAS----PDAACKSGTLPLHVAHYNDQKVALLLDQASPHAAANGYT 616
OY 127 PLIWAASAGEIETVRFLEWGDPHILAKERESALSLASTGYTDIVGLLEBRVDINITY 186
Db 617 PLHIAAKKQMDIATSLLEYGADANAATROGIAVHLAAQEGHVDWVSLLSRNANVLS 676
OY 187 DMNGSTPLIYAVRGHNVKCEVALLARGADLTTEADSGTTPMOLAVAGYRKQOVENHI 246
Db 677 NKSGTLPLHIAAQEDRVNAEVLVNOGAHVDAQTCKGYTPLHVCHYGNIKIVNLLQHS 736
OY 247 LKL 249
Db 737 AKV 739

RESULT 11
S2HUK
ankyrin 1, erythrocyte splice form 1 - human
N/Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N/Contains: ankyrin 2.2
C/Species: Homo sapiens (man)

C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C/Accession: S08275; A33219; PC2220; A35443
R. Lux, S.E.; John, K.M.; Bennett, V.
Nature 344, 36-42, 1990
A>Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure
A/Reference number: S08275, MUID:90158830, PMID:2137557
A/Accession: S08275
A/Molecule type: mRNA
A/Residues: 1-1881 <LU>
A/Cross-references: EMBL:X1609, NID:G28701, PIDN:CAA34610.1, PID:G28702
A/Accession: A33219
A/Molecule type: protein
A/Residues: 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30, 733-749, 'A', 751-753, 828-833, 'X', 835-855, 'X',
X', 1367, 1383-1427, 1601-1630, 1686-1698, 'D', 1700, 1763-1772 <LDX>
A/Note: 845-Arg and 1392-Thr were also found
R. Hermann, J.; Barel, M.; Prade, R.
Biochem. Biophys. Res. Commun. 204, 453-460, 1994
A>Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
A/Reference number: PC2220, MUID:95071348, PMID:7526850
A/Accession: PC2220
A/Molecule type: protein
A/Residues: 910-929 <HER>
R. Davis, L.H.; Bennett, V.
J. Biol. Chem. 265, 10589-10596, 1990
A>Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
A/Reference number: A35443; MUID:90285190; PMID:2141335
A/Accession: A35443
A/Molecule type: protein
A/Residues: 'X', 5, 'X', 7-12, 403-417, 'X', 419-422, 'H', 424, 'LQ', 797-800, 'L', 802-814, 862-863
C/Genetics:
A/Genes: GDB:ANK1, ANK
A/Cross-references: GDB:118737, OMIM:182900
A/Map position: 8p11.2-8p11.2
C/Superfamily: ankyrin; ankyrin repeat homology
C/Keywords: alternative splicing; phosphoprotein
F/2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
F/2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>
F/2-827/Domain: 89K #status predicted <DOM1>
F/44-76/Domain: anion exchange protein binding
F/77-109/Domain: ankyrin repeat homology <AN01>
F/110-142/Domain: ankyrin repeat homology <AN03>
F/143-171/Domain: ankyrin repeat homology <AN04>
F/112-204/Domain: ankyrin repeat homology <AN05>
F/205-237/Domain: ankyrin repeat homology <AN06>
F/228-270/Domain: ankyrin repeat homology <AN07>
F/271-303/Domain: ankyrin repeat homology <AN08>
F/304-336/Domain: ankyrin repeat homology <AN09>
F/337-369/Domain: ankyrin repeat homology <AN10>
F/370-402/Domain: ankyrin repeat homology <AN11>
F/403-435/Domain: ankyrin repeat homology <AN12>
F/436-468/Domain: ankyrin repeat homology <AN13>
F/469-501/Domain: ankyrin repeat homology <AN14>
F/502-534/Domain: ankyrin repeat homology <AN15>
F/535-567/Domain: ankyrin repeat homology <AN16>
F/568-600/Domain: ankyrin repeat homology <AN17>
F/601-633/Domain: ankyrin repeat homology <AN18>
F/634-666/Domain: ankyrin repeat homology <AN19>
F/667-699/Domain: ankyrin repeat homology <AN20>
F/700-732/Domain: ankyrin repeat homology <AN21>
F/733-765/Domain: ankyrin repeat homology <AN22>
F/766-798/Domain: ankyrin repeat homology <AN23>
F/828-1382/Domain: 62K #status predicted <DOM2>
F/828-1382/Region: Spectrin binding
F/1383-1881/Domain: 55K #status predicted <DOM3>

Query Match 13.7%; Score 184; DB 1; Length 1881;
Best Local Similarity 23.1%; Pred. No. 2.9e-06;
Matches 54; Conservative 37; Mismatches 69; Indels 74; Gaps 3;
OY 74 TNRQGNVEGALPATLDSTIHQLAAGELDQKEHLRKGDNLVVKPDGRGFTPLIWA 133
Db 73 TTTKGN-----TALHIALAAGDEVRELVNNGAN-VNAQSGKFTPLVMAQ 120

